



OIEP

RAW SEQUENCE LISTING

DATE: 02/05/2002

PATENT APPLICATION: US/10/044,543

TIME: 16:58:37

Input Set : A:\1144DSEQLIST.TXT

Output Set: N:\CRF3\02052002\J044543.raw

ENTERED

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4 <110> APPLICANT: Singletary, George
5   Zhou, Lan
7 <120> TITLE OF INVENTION: Novel Starch Synthase Polynucleotides
8   and Their Use in the Production of New Starches
11 <130> FILE REFERENCE: 1144D
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/044,543
C--> 13 <141> CURRENT FILING DATE: 2002-01-11
13 <150> PRIOR APPLICATION NUMBER: 09/388,743
14 <151> PRIOR FILING DATE: 1999-09-02
16 <160> NUMBER OF SEQ ID NOS: 28
18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2202
22 <212> TYPE: DNA
23 <213> ORGANISM: Curcuma zedoaria
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (130)...(1974)
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30 cactcatcac ttccgctgca agccagagag agaaagagcg atcgagctcc ggcggtgatt      60
31 ctctctcgca tctctgcttc tctctctctc tctctctttg atcgaagaga tcgccgtgag      120
32 ggtatcccc atg gcc atg cct tct gtg act gca tca cac ttc att gct aaa      171
33   Met Ala Met Pro Ser Val Thr Ala Ser His Phe Ile Ala Lys
34       1               5               10
36 acc cca tgc tcc agc tac aat gga gct agt gat ttg gag ggt ttg gcc      219
37 Thr Pro Cys Ser Ser Tyr Asn Gly Ala Ser Asp Leu Glu Gly Leu Ala
38   15               20               25               30
40 ttc caa atc aga agg atc cct tat ctg agt aac cat gcc agt act ttt      267
41 Phe Gln Ile Arg Arg Ile Pro Tyr Leu Ser Asn His Ala Ser Thr Phe
42       35               40               45
44 gaa gga ctg aga tcg cgg aac caa atg aat tca cgt cca atg cag tgt      315
45 Glu Gly Leu Arg Ser Arg Asn Gln Met Asn Ser Arg Pro Met Gln Cys
46       50               55               60
48 gca aag gca act act agg caa gtg agg aag gga atc caa cat gct agc      363
49 Ala Lys Ala Thr Thr Arg Gln Val Arg Lys Gly Ile Gln His Ala Ser
50       65               70               75
52 cga aga ccc tct gta atc tgt gca agt gga atg aac ttg atc ttt gtt      411
53 Arg Arg Pro Ser Val Ile Cys Ala Ser Gly Met Asn Leu Ile Phe Val
54       80               85               90
56 gct gct gag gtg gct ccg tgg agt aaa act gga ggg ctt ggt gat gtt      459
57 Ala Ala Glu Val Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp Val
58       95               100              105              110
60 ctt gga ggt ttg cca ccg gcc atg gcg gca aag gga cac agg gtg atg      507

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61	Leu Gly Gly Leu Pro Pro Ala Met Ala Ala Lys Gly His Arg Val Met	
62	115 120 125	
64	act ata gca ccg cga cat gac caa tac aaa gat gga tgg gat acg gct	555
65	Thr Ile Ala Pro Arg His Asp Gln Tyr Lys Asp Gly Trp Asp Thr Ala	
66	130 135 140	
68	gtc ttt gtc gag ttg aaa gtt ggt gat aga att gaa act gtt cgc ttt	603
69	Val Phe Val Glu Leu Lys Val Gly Asp Arg Ile Glu Thr Val Arg Phe	
70	145 150 155	
72	ttc cac tgc tac aaa agg gga gtt gat cgg gtg ttt gtg gat cac cct	651
73	Phe His Cys Tyr Lys Arg Gly Val Asp Arg Val Phe Val Asp His Pro	
74	160 165 170	
76	ctc ttc ctt gag aag gtt tgg gga aaa act gga gga aag ata tat ggt	699
77	Leu Phe Leu Glu Lys Val Trp Gly Lys Thr Gly Gly Lys Ile Tyr Gly	
78	175 180 185 190	
80	cct gtc aca aga act gat tat gaa gac aac cag cta agg ttc tgt ctt	747
81	Pro Val Thr Arg Thr Asp Tyr Glu Asp Asn Gln Leu Arg Phe Cys Leu	
82	195 200 205	
84	ctg tgt ttg gca act ctg gaa act cca agg gtt ctg aat ccc aac aat	795
85	Leu Cys Leu Ala Thr Leu Glu Thr Pro Arg Val Leu Asn Pro Asn Asn	
86	210 215 220	
88	aac aaa tat cat tct gga cca aaa ggt gaa gat tta ttc att gct aac	843
89	Asn Lys Tyr His Ser Gly Pro Lys Gly Glu Asp Leu Phe Ile Ala Asn	
90	225 230 235	
92	gat tgg cat act gct cta tta cct tgc tat tta aag acc att gta tat	891
93	Asp Trp His Thr Ala Leu Leu Pro Cys Tyr Leu Lys Thr Ile Val Tyr	
94	240 245 250	
96	caa gcc cat gga ata tac aaa aat gct aaa gtt gct ttc tgc att cat	939
97	Gln Ala His Gly Ile Tyr Lys Asn Ala Lys Val Ala Phe Cys Ile His	
98	255 260 265 270	
100	aat att gcg tat cag gga cgg ttt gcc ttt gaa gat ttt tcg cgt ctc	987
101	Asn Ile Ala Tyr Gln Gly Arg Phe Ala Phe Glu Asp Phe Ser Arg Leu	
102	275 280 285	
104	aat ctc cct gat aca ttc aag tct tct ttt gat ttc atc gat ggc tat	1035
105	Asn Leu Pro Asp Thr Phe Lys Ser Ser Phe Asp Phe Ile Asp Gly Tyr	
106	290 295 300	
108	gca aaa cca ata aaa gga agg aaa atc aac tgg atg aag gcg gga att	1083
109	Ala Lys Pro Ile Lys Gly Arg Lys Ile Asn Trp Met Lys Ala Gly Ile	
110	305 310 315	
112	ata gaa tca gat cgt gca ttg act gtg agc cca tac tat gcc cag gaa	1131
113	Ile Glu Ser Asp Arg Ala Leu Thr Val Ser Pro Tyr Tyr Ala Gln Glu	
114	320 325 330	
116	ctc gtc tca gga atc gat aag ggc gtc gag ttg gac aat ata ctg cgc	1179
117	Leu Val Ser Gly Ile Asp Lys Gly Val Glu Leu Asp Asn Ile Leu Arg	
118	335 340 345 350	
120	ttg aaa acc atc tgt ggc atc ata aat gga atg gac acc aac gag tgg	1227
121	Leu Lys Thr Ile Cys Gly Ile Ile Asn Gly Met Asp Thr Asn Glu Trp	
122	355 360 365	
124	aat ccc tca aca gac aaa tac ata aca gca aat tac gac gca acc act	1275
125	Asn Pro Ser Thr Asp Lys Tyr Ile Thr Ala Asn Tyr Asp Ala Thr Thr	

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126		370		375		380	
128	gta atg gag gca aag cca ctc aac aag gaa gct ttg caa gct gag gtt						1323
129	Val Met Glu Ala Lys Pro Leu Asn Lys Glu Ala Leu Gln Ala Glu Val						
130		385		390		395	
132	gga ctg ccc gtc aac agt aaa atc cct gtg ata gct ttc att ggc aga						1371
133	Gly Leu Pro Val Asn Ser Lys Ile Pro Val Ile Ala Phe Ile Gly Arg						
134		400		405		410	
136	cta gaa gaa caa aag ggt tca gac att cta gct gaa gca att cca aag						1419
137	Leu Glu Glu Gln Lys Gly Ser Asp Ile Leu Ala Glu Ala Ile Pro Lys						
138		415		420		425	430
140	ttc ttc gat cag gat gtt caa gtg ata gtt ctc ggt act ggt aaa aag						1467
141	Phe Phe Asp Gln Asp Val Gln Val Ile Val Leu Gly Thr Gly Lys Lys						
142		435		440		445	
144	aag tta gag cgc caa ctt gca ttg ctc gag gac gag ttc cca gac aaa						1515
145	Lys Leu Glu Arg Gln Leu Ala Leu Leu Glu Asp Glu Phe Pro Asp Lys						
146		450		455		460	
148	ttc aga gct cat atg aag ttc aat att cct ttg gct cat gga atc atg						1563
149	Phe Arg Ala His Met Lys Phe Asn Ile Pro Leu Ala His Gly Ile Met						
150		465		470		475	
152	gcg ggt gct gat atc ctt gtt att ccc agt agg ttc gaa cca tgc ggt						1611
153	Ala Gly Ala Asp Ile Leu Val Ile Pro Ser Arg Phe Glu Pro Cys Gly						
154		480		485		490	
156	ctc att cag ctc cag ggc atg aga tac gga acc cct tcc atg tgc acc						1659
157	Leu Ile Gln Leu Gln Gly Met Arg Tyr Gly Thr Pro Ser Met Cys Thr						
158		495		500		505	510
160	acg act ggt ggg ctc gtc gac act gtc aaa gaa ggc atc aca ggt ttc						1707
161	Thr Thr Gly Gly Leu Val Asp Thr Val Lys Glu Gly Ile Thr Gly Phe						
162		515		520		525	
164	cac atg ggt ccc ttc agt gtg gag tgc gac att gcc gac gag gcc gac						1755
165	His Met Gly Pro Phe Ser Val Glu Cys Asp Ile Ala Asp Glu Ala Asp						
166		530		535		540	
168	gtg cta aag att gtg gaa gca gtg aag aga gcc ctt atg gtt tat gga						1803
169	Val Leu Lys Ile Val Glu Ala Val Lys Arg Ala Leu Met Val Tyr Gly						
170		545		550		555	
172	acg cct gct ttc gag gag atg ata cag aac tgc atg gct caa gat ttc						1851
173	Thr Pro Ala Phe Glu Glu Met Ile Gln Asn Cys Met Ala Gln Asp Phe						
174		560		565		570	
176	tcc tgg aag ggg cca gca aag gaa tgg gag aag ttc ttg ctg agc ctt						1899
177	Ser Trp Lys Gly Pro Ala Lys Glu Trp Glu Lys Phe Leu Leu Ser Leu						
178		575		580		585	590
180	ggg ctc gag ggt agt gaa gct gga att gaa ggc gag gaa gta gct cct						1947
181	Gly Leu Glu Gly Ser Glu Ala Gly Ile Glu Gly Glu Glu Val Ala Pro						
182		595		600		605	
184	ctc gcc aag gaa aac gtg gcc act cca tgaaactgat catcgagttg						1994
185	Leu Ala Lys Glu Asn Val Ala Thr Pro						
186		610		615			
188	tgttcctcac tgcattttca caataaatgg tttgttaaat agtagagata tcatctatca						2054
189	ctgcaacgtg ttgtaaattt gttcttgtaa aataagccgt gtaattctaac tctaaggccg						2114
190	tttgttggcg taatgcagat gctatctgtt ttaattttta aaaaaaaaaa aaaaaaaaaa						2174

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194 <211> LENGTH: 615
195 <212> TYPE: PRT
196 <213> ORGANISM: Curcuma zedoaria
198 <400> SEQUENCE: 2
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200 1 5 10 15
201 Cys Ser Ser Tyr Asn Gly Ala Ser Asp Leu Glu Gly Leu Ala Phe Gln
202 20 25 30
203 Ile Arg Arg Ile Pro Tyr Leu Ser Asn His Ala Ser Thr Phe Glu Gly
204 35 40 45
205 Leu Arg Ser Arg Asn Gln Met Asn Ser Arg Pro Met Gln Cys Ala Lys
206 50 55 60
207 Ala Thr Thr Arg Gln Val Arg Lys Gly Ile Gln His Ala Ser Arg Arg
208 65 70 75 80
209 Pro Ser Val Ile Cys Ala Ser Gly Met Asn Leu Ile Phe Val Ala Ala
210 85 90 95
211 Glu Val Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp Val Leu Gly
212 100 105 110
213 Gly Leu Pro Pro Ala Met Ala Ala Lys Gly His Arg Val Met Thr Ile
214 115 120 125
215 Ala Pro Arg His Asp Gln Tyr Lys Asp Gly Trp Asp Thr Ala Val Phe
216 130 135 140
217 Val Glu Leu Lys Val Gly Asp Arg Ile Glu Thr Val Arg Phe Phe His
218 145 150 155 160
219 Cys Tyr Lys Arg Gly Val Asp Arg Val Phe Val Asp His Pro Leu Phe
220 165 170 175
221 Leu Glu Lys Val Trp Gly Lys Thr Gly Gly Lys Ile Tyr Gly Pro Val
222 180 185 190
223 Thr Arg Thr Asp Tyr Glu Asp Asn Gln Leu Arg Phe Cys Leu Leu Cys
224 195 200 205
225 Leu Ala Thr Leu Glu Thr Pro Arg Val Leu Asn Pro Asn Asn Asn Lys
226 210 215 220
227 Tyr His Ser Gly Pro Lys Gly Glu Asp Leu Phe Ile Ala Asn Asp Trp
228 225 230 235 240
229 His Thr Ala Leu Leu Pro Cys Tyr Leu Lys Thr Ile Val Tyr Gln Ala
230 245 250 255
231 His Gly Ile Tyr Lys Asn Ala Lys Val Ala Phe Cys Ile His Asn Ile
232 260 265 270
233 Ala Tyr Gln Gly Arg Phe Ala Phe Glu Asp Phe Ser Arg Leu Asn Leu
234 275 280 285
235 Pro Asp Thr Phe Lys Ser Ser Phe Asp Phe Ile Asp Gly Tyr Ala Lys
236 290 295 300
237 Pro Ile Lys Gly Arg Lys Ile Asn Trp Met Lys Ala Gly Ile Ile Glu
238 305 310 315 320
239 Ser Asp Arg Ala Leu Thr Val Ser Pro Tyr Tyr Ala Gln Glu Leu Val
240 325 330 335
241 Ser Gly Ile Asp Lys Gly Val Glu Leu Asp Asn Ile Leu Arg Leu Lys

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242          340          345          350
243 Thr Ile Cys Gly Ile Ile Asn Gly Met Asp Thr Asn Glu Trp Asn Pro
244          355          360          365
245 Ser Thr Asp Lys Tyr Ile Thr Ala Asn Tyr Asp Ala Thr Thr Val Met
246          370          375          380
247 Glu Ala Lys Pro Leu Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu
248          385          390          395          400
249 Pro Val Asn Ser Lys Ile Pro Val Ile Ala Phe Ile Gly Arg Leu Glu
250          405          410          415
251 Glu Gln Lys Gly Ser Asp Ile Leu Ala Glu Ala Ile Pro Lys Phe Phe
252          420          425          430
253 Asp Gln Asp Val Gln Val Ile Val Leu Gly Thr Gly Lys Lys Lys Leu
254          435          440          445
255 Glu Arg Gln Leu Ala Leu Leu Glu Asp Glu Phe Pro Asp Lys Phe Arg
256          450          455          460
257 Ala His Met Lys Phe Asn Ile Pro Leu Ala His Gly Ile Met Ala Gly
258          465          470          475          480
259 Ala Asp Ile Leu Val Ile Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile
260          485          490          495
261 Gln Leu Gln Gly Met Arg Tyr Gly Thr Pro Ser Met Cys Thr Thr Thr
262          500          505          510
263 Gly Gly Leu Val Asp Thr Val Lys Glu Gly Ile Thr Gly Phe His Met
264          515          520          525
265 Gly Pro Phe Ser Val Glu Cys Asp Ile Ala Asp Glu Ala Asp Val Leu
266          530          535          540
267 Lys Ile Val Glu Ala Val Lys Arg Ala Leu Met Val Tyr Gly Thr Pro
268          545          550          555          560
269 Ala Phe Glu Glu Met Ile Gln Asn Cys Met Ala Gln Asp Phe Ser Trp
270          565          570          575
271 Lys Gly Pro Ala Lys Glu Trp Glu Lys Phe Leu Leu Ser Leu Gly Leu
272          580          585          590
273 Glu Gly Ser Glu Ala Gly Ile Glu Gly Glu Glu Val Ala Pro Leu Ala
274          595          600          605
275 Lys Glu Asn Val Ala Thr Pro
276          610          615
278 <210> SEQ ID NO: 3
279 <211> LENGTH: 25
280 <212> TYPE: DNA
281 <213> ORGANISM: Curcuma zedoaria
283 <400> SEQUENCE: 3
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286 <210> SEQ ID NO: 4
287 <211> LENGTH: 25
288 <212> TYPE: DNA
289 <213> ORGANISM: Curcuma zedoaria
291 <400> SEQUENCE: 4
292 tcatggagtg gccacgtttt ccttg
294 <210> SEQ ID NO: 5
295 <211> LENGTH: 2348

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VERIFICATION SUMMARY

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Input Set : A:\1144DSEQLIST.TXT

Output Set: N:\CRF3\02052002\J044543.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date